IN THE SPECIFICATION:

Amendments to the Specification:

Replace the paragraph on page 1, lines 7-11, with the following paragraph:

This application is a continuation-in-part of co-pending USSN 09/561,811, filed on April 28, 2000, which claims the benefit of provisional application USSN 60/131,473, filed April 28, 1999. This application also claims priority to USSN 60/270,823, filed February 23, 2001; and to USSN 60/281,353, filed April 3, 2001. ~~The present application also claims priority to USSN 09/561,811, filed April 28, 2000, which claims the benefit of prior-filed provisional application USSN 60/131,473, filed April 28, 1999.~~ The contents of all of these patent applications are incorporated herein by this reference in their entirety.

Replace the paragraph on page 3, lines 15-32, with the following paragraph:

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 71 ~~65~~ to nucleotide 607 ~~601~~;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone IL-22 deposited under accession number ATCC 207231;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone IL-22 deposited under accession number ATCC 207231;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone IL-22 deposited under accession number ATCC 207231;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone IL-22 deposited under accession number ATCC 207231;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Replace the paragraph on page 4, lines 13-27, with the following paragraph:

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 71 ~~65~~ to nucleotide 607 ~~601~~; the nucleotide sequence of the full-length protein coding sequence of clone IL-22 deposited under accession number ATCC 207231; or the nucleotide sequence of a mature protein coding sequence of clone IL-22 deposited under accession number ATCC 207231 (*e.g.*, nucleotides 1-1177 of SEQ ID NO:1). In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone IL-22 deposited under accession number ATCC 207231 (*e.g.*, amino acids 1-179 of SEQ ID NO: 2). In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:2.

Replace the paragraph on page 5, lines 25-33 through page 6, lines 1-2, with the following paragraph:

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 71 ~~65~~ to nucleotide 607 ~~601~~, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 71 ~~65~~ to nucleotide 607 ~~601~~, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 71 ~~65~~ to nucleotide 607 ~~601~~.

Replace the paragraph on page 13, lines 8-21, with the following paragraph:

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. The corresponding chromosomal location for a disclosed polynucleotide can be determined by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information. ~~having the address http://www.ncbi.nlm.nih.gov/UniGene/, in order to identify "UniGene clusters" of overlapping sequences.~~ Many of the "UniGene clusters" of overlapping sequences ~~so identified~~ will already have been mapped to particular chromosomal sites.

Replace the paragraph on page 21, lines 3-12, with the following paragraph:

The protein of the invention can be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin- TOYOPEARL™ ~~toyopearl®~~ or Cibacrom blue 3GA SEPHAROSE™ ~~Sepharose®~~; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Replace the paragraph on page 29, lines 5-24, with the following paragraph:

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, surfactant carriers as CREMOPHOR EL™ ~~Cremophor EL™~~ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that

easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Replace the paragraph on page 63, lines 7-11, with the following paragraph:

> mRNA were analyzed on the Murine 74k (Mu74K) chip set. The data was reduced with the use of ~~GENECHIP~~ GENECHIP™ 4.0 software. Each experimental sample was compared to a time matched control in a two-file analysis. The data were filtered with the criteria for genes that were called "Present" in one group, and removing all genes that were not called either "Increasing" or "Decreasing".